



IFWO

## RAW SEQUENCE LISTING

DATE: 07/26/2004

PATENT APPLICATION: US/10/786,445A

TIME: 15:28:04

Input Set : A:\096429-9141.txt

Output Set: N:\CRF4\07262004\J786445A.raw

3 <110> APPLICANT: Welch, Rodney A.  
 4 Lathem, Wyndham W.  
 5 Grys, Thomas E.  
 7 <120> TITLE OF INVENTION: E. COLI O157:H7 C1-INH-BINDING PROTEIN AND METHODS OF USE  
 9 <130> FILE REFERENCE: 096429-9141  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/786,445A  
 12 <141> CURRENT FILING DATE: 2004-02-25  
 14 <150> PRIOR APPLICATION NUMBER: 10/002,309  
 15 <151> PRIOR FILING DATE: 2001-10-26  
 17 <150> PRIOR APPLICATION NUMBER: 60/243,675  
 18 <151> PRIOR FILING DATE: 2000-10-26  
 20 <160> NUMBER OF SEQ ID NOS: 25  
 22 <170> SOFTWARE: PatentIn version 3.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 2798  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Unknown  
 29 <220> FEATURE:  
 30 <223> OTHER INFORMATION: Description of Unknown Organism: E. coli O157:H7 plasmid  
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 32 <220> FEATURE:  
 33 <221> NAME/KEY: CDS  
 34 <222> LOCATION: (138)..(2798)  
 35 <223> OTHER INFORMATION:  
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 41 ctgaaaaaat aaaatataga aatactgtta tatccggctg catgaacact aaaatgaatg 120  
 43 agagatggag aacaccg atg aaa tta aag tat ctg tca tgt acg atc ctt 170  
 44 Met Lys Leu Lys Tyr Leu Ser Cys Thr Ile Leu  
 45 1 5 10  
 47 gcc cct ctg gcg att ggg gta ttt tct gca aca gct gct gat aat aat 218  
 48 Ala Pro Leu Ala Ile Gly Val Phe Ser Ala Thr Ala Ala Asp Asn Asn  
 49 15 20 25  
 51 tca gcc att tat ttc aat acc tcc cag cct ata aat gat ctg cag ggt 266  
 52 Ser Ala Ile Tyr Phe Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly  
 53 30 35 40  
 55 tcg ttg gcc gca gag gtg aaa ttt gca caa agc cag att tta ccc gcc 314  
 56 Ser Leu Ala Ala Glu Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala  
 57 45 50 55  
 59 cat cct aaa gaa ggg gat agt caa cca cat ctg acc agc ctg cgg aaa 362  
 60 His Pro Lys Glu Gly Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys  
 61 60 65 70 75  
 63 agt ctg ctg ctt gtc cgt ccg gtg aaa gct gat gat aaa aca cct gtt 410  
 64 Ser Leu Leu Leu Val Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val



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65	80	85	90	
67	cag gtg gaa gcc cgc gat gat aat aat aaa att ctc ggt acg tta acc	458		
68	Gln Val Glu Ala Arg Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr			
69	95 100 105			
71	ctt tat cct cct tca tca cta ccg gat aca atc tac cat ctg gat ggt	506		
72	Leu Tyr Pro Pro Ser Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly			
73	110 115 120			
75	gtt ccg gaa ggt ggt atc gat ttc aca cct cat aat gga acg aaa aag	554		
76	Val Pro Glu Gly Gly Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys			
77	125 130 135			
79	atc att aat acg gtg gct gaa gta aac aaa ctc agt gat gcc agc ggg	602		
80	Ile Ile Asn Thr Val Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly			
81	140 145 150 155			
83	agt tct att cat agc cat cta aca aat aat gca ctg gtg gag atc cat	650		
84	Ser Ser Ile His Ser His Leu Thr Asn Asn Ala Leu Val Glu Ile His			
85	160 165 170			
87	act gca aat ggt cgt tgg gta aga gac att tat ctg ccg cag gga ccc	698		
88	Thr Ala Asn Gly Arg Trp Val Arg Asp Ile Tyr Leu Pro Gln Gly Pro			
89	175 180 185			
91	gac ctt gaa ggt aag atg gtt cgc ttt gtt tgc tct gca ggc tat agt	746		
92	Asp Leu Glu Gly Lys Met Val Arg Phe Val Ser Ser Ala Gly Tyr Ser			
93	190 195 200			
95	tca acg gtt ttt tat ggt gat cga aaa gtc aca ctc tgc gtg ggt aac	794		
96	Ser Thr Val Phe Tyr Gly Asp Arg Lys Val Thr Leu Ser Val Gly Asn			
97	205 210 215			
99	act ctt ctg ttc aaa tat gta aat ggt cag tgg ttc cgc tcc ggt gaa	842		
100	Thr Leu Leu Phe Lys Tyr Val Asn Gly Gln Trp Phe Arg Ser Gly Glu			
101	220 225 230 235			
103	ctg gag aat aat cga atc act tat gct cag cat att tgg agt gct gaa	890		
104	Leu Glu Asn Asn Arg Ile Thr Tyr Ala Gln His Ile Trp Ser Ala Glu			
105	240 245 250			
107	ctg cct gcg cac tgg atc gtg cct ggt tta aac ttg gtg att aaa cag	938		
108	Leu Pro Ala His Trp Ile Val Pro Gly Leu Asn Leu Val Ile Lys Gln			
109	255 260 265			
111	ggc aat ctg agc ggt cgc cta aat gat atc aag att gga gca ccg ggt	986		
112	Gly Asn Leu Ser Gly Arg Leu Asn Asp Ile Lys Ile Gly Ala Pro Gly			
113	270 275 280			
115	gag ctg ttg ttg cat aca att gat atc ggg atg ttg acc act ccc ccg	1034		
116	Glu Leu Leu Leu His Thr Ile Asp Ile Gly Met Leu Thr Thr Pro Arg			
117	285 290 295			
119	gat cgc ttt gat ttt gcc aaa gac aaa gaa gca cat agg gaa tat ttc	1082		
120	Asp Arg Phe Asp Phe Ala Lys Asp Lys Glu Ala His Arg Glu Tyr Phe			
121	300 305 310 315			
123	cag acc att cct gta agt cgt atg att gtt aat aat tat gcg cct cta	1130		
124	Gln Thr Ile Pro Val Ser Arg Met Ile Val Asn Asn Tyr Ala Pro Leu			
125	320 325 330			
127	cac cta aag gaa gtt atg tta cca acc gga gag tta ttg aca gat atg	1178		
128	His Leu Lys Glu Val Met Leu Pro Thr Gly Glu Leu Leu Thr Asp Met			
129	335 340 345			

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131	gat	cca	gga	aat	ggt	ggg	tgg	cat	agt	ggt	aca	atg	cgt	caa	aga	ata	1226
132	Asp	Pro	Gly	Asn	Gly	Gly	Trp	His	Ser	Gly	Thr	Met	Arg	Gln	Arg	Ile	
133			350					355						360			
135	ggt	aaa	gaa	ttg	gtt	tgc	cat	ggc	att	gat	aat	gct	aac	tat	ggt	tta	1274
136	Gly	Lys	Glu	Leu	Val	Ser	His	Gly	Ile	Asp	Asn	Ala	Asn	Tyr	Gly	Leu	
137			365					370						375			
139	aat	agt	acc	gca	ggc	tta	ggg	gag	aat	agt	cat	cca	tat	gta	gtt	gcg	1322
140	Asn	Ser	Thr	Ala	Gly	Leu	Gly	Glu	Asn	Ser	His	Pro	Tyr	Val	Val	Ala	
141	380						385					390				395	
143	caa	tta	gcg	gca	cat	aat	agc	cgc	ggt	aat	tat	gct	aat	ggc	atc	cag	1370
144	Gln	Leu	Ala	Ala	His	Asn	Ser	Arg	Gly	Asn	Tyr	Ala	Asn	Gly	Ile	Gln	
145					400					405					410		
147	gtt	cat	ggt	ggc	tcc	gga	ggt	ggg	gga	att	gtt	act	tta	gat	tcc	aca	1418
148	Val	His	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ile	Val	Thr	Leu	Asp	Ser	Thr	
149				415					420					425			
151	ttg	ggg	aat	gag	ttc	agt	cat	gaa	gtt	ggt	cat	aat	tat	ggt	ctt	ggt	1466
152	Leu	Gly	Asn	Glu	Phe	Ser	His	Glu	Val	Gly	His	Asn	Tyr	Gly	Leu	Gly	
153			430					435						440			
155	cat	tat	gta	gat	ggt	ttc	aag	ggt	tct	gta	cat	cgt	agt	gca	gaa	aat	1514
156	His	Tyr	Val	Asp	Gly	Phe	Lys	Gly	Ser	Val	His	Arg	Ser	Ala	Glu	Asn	
157			445				450							455			
159	aac	aac	tca	act	tgg	gga	tgg	gat	ggt	gat	aaa	aaa	cgg	ttt	att	cct	1562
160	Asn	Asn	Ser	Thr	Trp	Gly	Trp	Asp	Gly	Asp	Lys	Lys	Arg	Phe	Ile	Pro	
161	460					465				470						475	
163	aac	ttt	tat	ccg	tct	caa	aca	aat	gaa	aag	agt	tgt	ctg	aat	aat	cag	1610
164	Asn	Phe	Tyr	Pro	Ser	Gln	Thr	Asn	Glu	Lys	Ser	Cys	Leu	Asn	Asn	Gln	
165				480						485						490	
167	tgt	caa	gaa	ccg	ttt	gat	gga	cac	aaa	ttt	ggt	ttt	gac	gcc	atg	gcg	1658
168	Cys	Gln	Glu	Pro	Phe	Asp	Gly	His	Lys	Phe	Gly	Phe	Asp	Ala	Met	Ala	
169				495					500					505			
171	gga	ggc	agc	cct	ttc	tct	gct	gca	aac	cgt	ttc	aca	atg	tat	act	ccg	1706
172	Gly	Gly	Ser	Pro	Phe	Ser	Ala	Ala	Asn	Arg	Phe	Thr	Met	Tyr	Thr	Pro	
173			510					515						520			
175	aat	tca	tgc	gct	atc	atc	cag	cgt	ttt	ttt	gaa	aat	aaa	gct	gtg	ttc	1754
176	Asn	Ser	Ser	Ala	Ile	Ile	Gln	Arg	Phe	Phe	Glu	Asn	Lys	Ala	Val	Phe	
177			525				530							535			
179	gat	agc	cgt	tcc	tcc	acc	ggc	ttc	agc	aag	tgg	aat	gca	gat	acg	cag	1802
180	Asp	Ser	Arg	Ser	Ser	Thr	Gly	Phe	Ser	Lys	Trp	Asn	Ala	Asp	Thr	Gln	
181	540					545						550				555	
183	gaa	atg	gaa	ccg	tat	gaa	cac	acc	att	gac	cgt	gcg	gag	cag	att	acg	1850
184	Glu	Met	Glu	Pro	Tyr	Glu	His	Thr	Ile	Asp	Arg	Ala	Glu	Gln	Ile	Thr	
185				560						565						570	
187	gct	tca	gtc	aat	gag	cta	agt	gaa	agc	aaa	atg	gct	gag	ctg	atg	gca	1898
188	Ala	Ser	Val	Asn	Glu	Leu	Ser	Glu	Ser	Lys	Met	Ala	Glu	Leu	Met	Ala	
189				575						580						585	
191	gag	tac	gct	gtc	gtc	aaa	gtg	cat	atg	tgg	aac	ggt	aac	tgg	aca	aga	1946
192	Glu	Tyr	Ala	Val	Val	Lys	Val	His	Met	Trp	Asn	Gly	Asn	Trp	Thr	Arg	
193			590					595						600			
195	aac	atc	tat	atc	cct	aca	gcc	tcc	gca	gat	aat	aga	ggc	agt	atc	ctg	1994

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196	Asn	Ile	Tyr	Ile	Pro	Thr	Ala	Ser	Ala	Asp	Asn	Arg	Gly	Ser	Ile	Leu	
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200	Thr	Ile	Asn	His	Glu	Ala	Gly	Tyr	Asn	Ser	Tyr	Leu	Phe	Ile	Asn	Gly	
201	620					625					630					635	
203	gac	gaa	aag	gtc	gtt	tcc	cag	ggg	tat	aaa	aag	agc	ttt	gtt	tcc	gat	2090
204	Asp	Glu	Lys	Val	Val	Ser	Gln	Gly	Tyr	Lys	Lys	Ser	Phe	Val	Ser	Asp	
205				640					645						650		
207	ggg	cag	ttc	tgg	aaa	gaa	cgt	gat	gtg	gtt	gat	act	cgt	gaa	gcg	cgt	2138
208	Gly	Gln	Phe	Trp	Lys	Glu	Arg	Asp	Val	Val	Asp	Thr	Arg	Glu	Ala	Arg	
209				655					660					665			
211	aag	cca	gag	cag	ttt	ggg	gtt	cct	gtg	acg	acc	ctg	gtg	ggg	tat	tac	2186
212	Lys	Pro	Glu	Gln	Phe	Gly	Val	Pro	Val	Thr	Thr	Leu	Val	Gly	Tyr	Tyr	
213			670					675					680				
215	gat	ccg	gaa	ggc	acg	ctg	tca	agc	tac	atc	tat	cct	gcg	atg	tat	ggg	2234
216	Asp	Pro	Glu	Gly	Thr	Leu	Ser	Ser	Tyr	Ile	Tyr	Pro	Ala	Met	Tyr	Gly	
217		685				690						695					
219	gcc	tat	ggc	ttc	act	tat	tcc	gat	gat	agt	cag	aat	cta	tcc	gat	aac	2282
220	Ala	Tyr	Gly	Phe	Thr	Tyr	Ser	Asp	Asp	Ser	Gln	Asn	Leu	Ser	Asp	Asn	
221	700				705					710					715		
223	gac	tgc	cag	ctg	cag	gtg	gat	acg	aaa	gaa	ggg	cag	ttg	cga	ttc	aga	2330
224	Asp	Cys	Gln	Leu	Gln	Val	Asp	Thr	Lys	Glu	Gly	Gln	Leu	Arg	Phe	Arg	
225				720					725					730			
227	ctg	gct	aat	cac	cgg	gct	aac	aac	act	gta	atg	aat	aag	ttc	cat	att	2378
228	Leu	Ala	Asn	His	Arg	Ala	Asn	Asn	Thr	Val	Met	Asn	Lys	Phe	His	Ile	
229				735					740					745			
231	aac	gtg	cca	aca	gaa	agt	cag	ccc	aca	cag	gcc	aca	ttg	gtt	tgc	aat	2426
232	Asn	Val	Pro	Thr	Glu	Ser	Gln	Pro	Thr	Gln	Ala	Thr	Leu	Val	Cys	Asn	
233			750					755					760				
235	aac	aag	ata	ctg	gat	acc	aaa	tgc	ctc	aca	cct	gcg	cca	gaa	gga	ctt	2474
236	Asn	Lys	Ile	Leu	Asp	Thr	Lys	Ser	Leu	Thr	Pro	Ala	Pro	Glu	Gly	Leu	
237		765				770					775						
239	acc	tat	act	gta	aat	ggg	cag	gca	ctt	cca	gca	aaa	gaa	aac	gag	gga	2522
240	Thr	Tyr	Thr	Val	Asn	Gly	Gln	Ala	Leu	Pro	Ala	Lys	Glu	Asn	Glu	Gly	
241	780				785					790					795		
243	tgc	atc	gtg	tcc	gtg	aat	tca	ggg	aaa	cgt	tac	tgt	ttg	ccg	gtt	ggg	2570
244	Cys	Ile	Val	Ser	Val	Asn	Ser	Gly	Lys	Arg	Tyr	Cys	Leu	Pro	Val	Gly	
245				800					805					810			
247	caa	cgg	tca	gga	tat	agc	ctt	cct	gac	tgg	att	gtt	ggg	cag	gaa	gtc	2618
248	Gln	Arg	Ser	Gly	Tyr	Ser	Leu	Pro	Asp	Trp	Ile	Val	Gly	Gln	Glu	Val	
249				815					820					825			
251	tat	gtc	gac	agc	ggg	gct	aaa	gcg	aaa	gtg	ctg	ctt	tct	gac	tgg	gat	2666
252	Tyr	Val	Asp	Ser	Gly	Ala	Lys	Ala	Lys	Val	Leu	Leu	Ser	Asp	Trp	Asp	
253			830					835					840				
255	aac	ctg	tcc	tat	aac	agg	att	ggg	gag	ttt	gta	ggg	aat	gtg	aac	cca	2714
256	Asn	Leu	Ser	Tyr	Asn	Arg	Ile	Gly	Glu	Phe	Val	Gly	Asn	Val	Asn	Pro	
257		845				850						855					
259	gct	gat	atg	aaa	aaa	gtt	aaa	gcc	tgg	aac	gga	cag	tat	ttg	gac	ttc	2762
260	Ala	Asp	Met	Lys	Lys	Val	Lys	Ala	Trp	Asn	Gly	Gln	Tyr	Leu	Asp	Phe	

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261 860 865 870 875 2798

263 agt aaa cct agg tca atg agg gtt gta tat aaa taa

264 Ser Lys Pro Arg Ser Met Arg Val Val Tyr Lys

265 880 885

268 <210> SEQ ID NO: 2

269 <211> LENGTH: 886

270 <212> TYPE: PRT

271 <213> ORGANISM: Unknown

273 <220> FEATURE:

274 <223> OTHER INFORMATION: Description of Unknown Organism: E. coli O157:H7 plasmid

p0157

276 <400> SEQUENCE: 2

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279 1 5 10 15

282 Gly Val Phe Ser Ala Thr Ala Ala Asp Asn Asn Ser Ala Ile Tyr Phe

283 20 25 30

286 Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly Ser Leu Ala Ala Glu

287 35 40 45

290 Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala His Pro Lys Glu Gly

291 50 55 60

294 Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys Ser Leu Leu Leu Val

295 65 70 75 80

298 Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val Gln Val Glu Ala Arg

299 85 90 95

302 Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr Leu Tyr Pro Pro Ser

303 100 105 110

306 Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly Val Pro Glu Gly Gly

307 115 120 125

310 Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys Ile Ile Asn Thr Val

311 130 135 140

314 Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly Ser Ser Ile His Ser

315 145 150 155 160

318 His Leu Thr Asn Asn Ala Leu Val Glu Ile His Thr Ala Asn Gly Arg

319 165 170 175

322 Trp Val Arg Asp Ile Tyr Leu Pro Gln Gly Pro Asp Leu Glu Gly Lys

323 180 185 190

326 Met Val Arg Phe Val Ser Ser Ala Gly Tyr Ser Ser Thr Val Phe Tyr

327 195 200 205

330 Gly Asp Arg Lys Val Thr Leu Ser Val Gly Asn Thr Leu Leu Phe Lys

331 210 215 220

334 Tyr Val Asn Gly Gln Trp Phe Arg Ser Gly Glu Leu Glu Asn Asn Arg

335 225 230 235 240

338 Ile Thr Tyr Ala Gln His Ile Trp Ser Ala Glu Leu Pro Ala His Trp

339 245 250 255

342 Ile Val Pro Gly Leu Asn Leu Val Ile Lys Gln Gly Asn Leu Ser Gly

343 260 265 270

346 Arg Leu Asn Asp Ile Lys Ile Gly Ala Pro Gly Glu Leu Leu Leu His

347 275 280 285

350 Thr Ile Asp Ile Gly Met Leu Thr Thr Pro Arg Asp Arg Phe Asp Phe

351 290 295 300

**VERIFICATION SUMMARY**

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L:11 M:270 C: Current Application Number differs, Wrong Format

L:38 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:35

L:700 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:18,Line#:697